REMARKS

Claims 1-8, 12-16, and 22 are now pending, with claim 1 being the sole independent claim.

Claims 9-11 and 17-21 have been canceled without prejudice to or disclaimer of the subject matter recited therein. Claims 1-7, 13, 15 and 16 have been amended. Claim 22 has been added. Two paragraphs of the specification have been amended to remove hyperlinks. No new matter has been added.

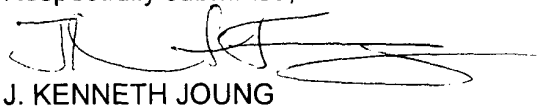
RESPONSE TO RESTRICTION REQUIREMENT

Applicants hereby elect, without traverse, the subject matter of Group I and SEQ ID NO:3 and SEQ ID NO:4. Applicants submit that the pending claims are all within Group I.

Please charge any fees or credit any overpayment of fees which are required in connection herewith to Deposit Account No. 04-1928 (E. I. du Pont de Nemours and Company).

In view of the foregoing, allowance of the above-referenced application is respectfully requested.

Respectfully submitted,



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VERSION WITH MARKINGS TO SHOW CHANGES MADE

In showing the changes, deleted material is shown brackets, and inserted material is shown underlined.

IN THE SPECIFICATION:

paragraph at page 9, lines 8-30

A "substantial portion" of an amino acid or nucleotide sequence comprises an amino acid or a nucleotide sequence that is sufficient to afford putative identification of the protein or gene that the amino acid or nucleotide sequence comprises. Amino acid and nucleotide sequences can be evaluated either manually by one skilled in the art, or by using computer-based sequence comparison and identification tools that employ algorithms such as BLAST (Basic Local Alignment Search Tool; Altschul et al. (1993) *J. Mol. Biol. 215*:403-410[; see also www.ncbi.nlm.nih.gov/BLAST/]). In general, a sequence of ten or more contiguous amino acids or thirty or more contiguous nucleotides is necessary in order to putatively identify a polypeptide or nucleic acid sequence as homologous to a known protein or gene. Moreover, with respect to nucleotide sequences, gene-specific oligonucleotide probes comprising 30 or more contiguous nucleotides may be used in sequence-dependent methods of gene identification (e.g., Southern hybridization) and isolation (e.g., *in situ* hybridization of bacterial colonies or bacteriophage plaques). In addition, short oligonucleotides of 12 or more nucleotides may be used as amplification primers in PCR in order to obtain a particular nucleic acid fragment comprising the primers. Accordingly, a "substantial portion" of a nucleotide sequence comprises a nucleotide sequence that will afford specific identification and/or isolation of a nucleic acid fragment comprising the sequence. The instant specification teaches amino acid and nucleotide sequences encoding polypeptides that comprise one or more particular plant proteins. The skilled artisan, having the benefit of the sequences as reported herein, may now use all or a substantial portion of the disclosed sequences for purposes known to those skilled in this art. Accordingly, the instant invention comprises the complete sequences as reported in the accompanying Sequence Listing, as well as substantial portions of those sequences as defined above.

paragraph at page 22, line 27 through page 23, line 6

cDNA clones encoding defensins were identified by conducting BLAST (Basic Local Alignment Search Tool; Altschul et al. (1993) *J. Mol. Biol. 215*:403-410[; see also www.ncbi.nlm.nih.gov/BLAST/]) searches for similarity to sequences contained

in th BLAST "nr" database (comprising all non-redundant GenBank CDS translations, sequences derived from the 3-dimensional structure Brookhaven Protein Data Bank, the last major release of the SWISS-PROT protein sequence database, EMBL, and DDBJ databases). The cDNA sequences obtained in Example 1 were analyzed for similarity to all publicly available DNA sequences contained in the "nr" database using the BLASTN algorithm provided by the National Center for Biotechnology Information (NCBI). The DNA sequences were translated in all reading frames and compared for similarity to all publicly available protein sequences contained in the "nr" database using the BLASTX algorithm (Gish and States (1993) *Nat. Genet. 3*:266-272) provided by the NCBI. For convenience, the P-value (probability) of observing a match of a cDNA sequence to a sequence contained in the searched databases merely by chance as calculated by BLAST are reported herein as "pLog" values, which represent the negative of the logarithm of the reported P-value. Accordingly, the greater the pLog value, the greater the likelihood that the cDNA sequence and the BLAST "hit" represent homologous proteins.

IN THE CLAIMS:

1. (amended) An isolated polynucleotide comprising:
   (a) a nucleotide sequence encoding a polypeptide having defensin activity, wherein the amino acid sequence of the polypeptide and the amino acid sequence of [SEQ ID NO:2,]SEQ ID NO:4[, SEQ ID NO:6, SEQ ID NO:8, or SEQ ID NO:10] have at least 80% sequence identity based on the Clustal alignment method, or
   (b) the complement of the nucleotide sequence.

2. (amended)The isolated polynucleotide of Claim 1, wherein the amino acid sequence of the polypeptide and the amino acid sequence of [SEQ ID NO:2,]SEQ ID NO:4[, SEQ ID NO:6, SEQ ID NO:8, or SEQ ID NO:10] have at least 85% sequence identity based on the Clustal alignment method.

3. (amended)The isolated polynucleotide of Claim 1, wherein the amino acid sequence of the polypeptide and the amino acid sequence of [SEQ ID NO:2,]SEQ ID NO:4[, SEQ ID NO:6, SEQ ID NO:8, or SEQ ID NO:10] have at least 90% sequence identity based on the Clustal alignment method.

4. (amended)The isolated polynucleotide of Claim 1, wherein the amino acid sequence of the polypeptide and the amino acid sequence of [SEQ ID NO:2,]SEQ ID NO:4[, SEQ ID NO:6, SEQ ID NO:8, or SEQ ID NO:10] have at least 95% sequence identity based on the Clustal alignment method.

5. (amended)The isolated polynucleotide of Claim 1, wherein the amino acid sequence of the polypeptide comprises the amino acid sequence of [SEQ ID NO:2,]SEQ ID NO:4[, SEQ ID NO:6, SEQ ID NO:8, or SEQ ID NO:10].

6. (amended)The isolated polynucleotide of Claim 1, wherein the nucleotide sequence comprises the nucleotide sequence of [SEQ ID NO:1,]SEQ ID NO:3[, SEQ ID NO:5, SEQ ID NO:7, or SEQ ID NO:9].

7. (amended)A recombinant DNA construct [chimeric gene] comprising the polynucleotide of Claim 1 operably linked to at least one [a] regulatory sequence.

13. (amended)A cell comprising the recombinant DNA construct [chimeric gene] of Claim 7.

15. (amended)A plant comprising the recombinant DNA construct [chimeric gene] of Claim 7.

16. (amended)A seed comprising the recombinant DNA construct [chimeric gene] of Claim 7.